FAME

User Manual for Version 2.1

2016

FAME can be downloaded from:
http://www.peternell.org/archive.html
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Chapter 1

Introduction

FAME (Fabric Analyser based Microstructure Evaluation) is a MATLAB®-based software for processing data recorded by an automatic fabric analyser microscope (Hammes and Peternell, in press). More details about the Fabric Analyser microscope (Russel-Head Instruments, Templestowe, Australia) are found in Wilson et al. (2003, 2007) and Peternell et al. (2011).

FAME is based on the original work of Peternell et al. (2014), a suite of MATLAB® scripts that utilize the MATLAB® open-source toolboxes MTEX (Bachmann et al., 2011) and PolyLX (optional; Lexa, 2003). These scripts were further improved and a couple of new features were added. We added a graphical user interface (GUI) to make FAME more user-friendly and offer a compiled standalone version to run on Microsoft® operation systems. A MATLAB® licence is not needed.

This manual is intended to introduce the user into the FAME software. It also tries to cover all aspects of FAME, without going into too much into detail about the used algorithms. The interested reader is asked to read Hammes and Peternell (in press) and Peternell et al. (2014).

In chapter 6 the complete graphical user interface of FAME is described and all buttons and panels are discussed in detail. For each major process this manual offers a workflow, accompanied by a “how to...?” step-by-step guide, together with two examples (“TutEx”, “DefEx”); simple, but still realistic data sets (chapter 3). To begin with the tutorial, the reader is referred to start at figure 13 and then follow the FAME processes step-by-step. An overview of the different FAME steps and their internal connections is shown in figures 3 and 4. In the workflow the instructions for the tutorial example are written in green, marked with a “T” at the beginning. All necessary input parameters, the approximately required time of the processes and the name of output files are indicated there. After the user completed the tutorial, (s)he should be able to process her/his own data.
The developers appreciate any comment about FAME (or this manual), and in particular about encountered problems or improvements.

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Chapter 2

Copyright

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Chapter 3

A note about the examples

For the tutorial we have chosen 2 sample data sets ("TutEx": Tutorial example, "DefEx": Deformation example).

To introduce into the FAME single analysis we use part of a quartzite thin section from Mt. Isa, Australia that was scanned with a Fabric Analyser G50 ("TutEx"; Fig. 1a).

Figure 1: The tutorial example ("TutEx"), Mt. Isa quartzite. Fabric Analyser G50 orientation image (a) and related FAME grain map (b). FAME “analysing data” parameters are: Reduce data=2, gqgm/rqgm=1, min. rad.=56.67, angle gr. crit.=4.11, step growth activated (5 steps, threshold=5). Long side of the image is 400 pixels (2.5mm).

To illustrate the FAME applied to batch data, single steps from an 2d in situ $D_2O$ ice deformation experiment were selected ("DefEx2"; Fig. 2a, b; Peternell et al., 2014). The initial 5mmx5mm sized sample was deformed with a strain rate of $2.5\cdot10^{-6}\frac{1}{s}$ at $-7^\circ$C. To decrease the processing time, 10
out of 321 slides were chosen and then a 400x400 pixels (2mmx2mm) area selected.

Figure 2: Fabric Analyser Orientation images (upper row) and corresponding FAME grain maps (bottom row) of a *in situ* deformation experiment of $D_2O$ ice (“DefEx”). Section shown before (a) and after deformation (b). FAME “analysing data” parameters are: Reduce data=10, gqgm/rqgm=1, min. rad.=45, angle gr. crit.=3.56, angle gr. crit. after def.=5.3, step growth activated (8 steps, threshold=7). Size of each frame is 1120x1120 pixels (5.6mmx5.6mm)
Chapter 4

Installation

The latest FAME version can be downloaded from:

http://www.peternell.org/archive.html

FAME doesn’t require MATLAB® to run. Only the .exe-file of FAME and the MATLAB® Compiler Runtime (MCR, version 2012a) are necessary. The latter is freely available from:

http://www.mathworks.com/products/compiler/

Hints about the installation and information about the needed version can be found in the readme.txt file. If MATLAB® is fully installed (version 2012a required!), the MCR is not necessary.

After the successful installation of the MCR, FAME can be started by simply open the FAME.exe file. In case of problems regarding user rights, we recommend to start FAME using the “run as administrator”-option in Windows.
Chapter 5

Overview

Figures 3 and 4 show the general workflow of FAME.

Figure 3: General FAME workflow.
FAME is mainly divided into three parts: “Loading data”, “analysing data” and data output (Fig. 3). The first process loads the data into a FAME-supported data structure and the second performs the grain labelling. Subsequently the results can be used for plotting diagrams (statistics, chapter 9) or converted to a format supported by the elle modelling-software (FAME2elle, chapter 10).

To assist the user during analysis, panels and buttons of already accomplished or forthcoming processes are inaccessible. For example, the panels regarding the analysis process only become available after data was successfully loaded.

The individual processes will be represented as separate workflows in the following chapters.

Figure 4: Simplified workflow of FAME, illustrated on the main GUI. Numbers refer to the respective FAME steps in figure 3.

5.1 Log file

All events such as “end of a process”, possible errors etc. are recorded with a timestamp in a log.txt file. This is in particular useful for estimating processing time. The log file is stored in a log-folder next to the Fabric Analyser data. For 2d deformation experiments the folder is located in the first subfolder (in general “0001”). If the log-folder and -file are not already present, they will be automatically created by FAME.
Chapter 6

Graphical user interface

In this chapter all FAME graphical user interfaces (GUI’S) are introduced. The panels are numbered continuously and explained in the following lists. Numbers in square brackets (“[]”) in the following chapters refer to these lists.

6.1 Main GUI

The main GUI (Fig. 5) is the central element of FAME. It incorporates the “loading data”, “analysing data” and “output data” structure. It also leads the user to the various sub GUI’s.

1. new project: Select a Fabric Analyser data.cis-file to initialise a new FAME project. Don’t forget to decide if you want to analyse single or 2d deformation experiment data (see [3]: 2d deformation experiment). In the latter case its irrelevant which of the multiple .cis files is selected.

2. open project: Opens a existing project. Select a mtex_import_n_data.mat (n: reduce data parameter, [5]) file if the data was only loaded previously or a results... .mat (filename containing information about the used parameters) file to open already analysed data.

3. 2d deformation experiment: For analysing in-situ deformation data consisting of multiple Fabric Analyser recordings. Switch off if only single data is used. Needs to be selected previously if a new project is initialised.

4. path: Path to Fabric Analyser data files (data.cis and info.txt). For deformation experiments the path leads to the parent folder. The path is in general selected by open a new or already existing project ([1], [2]), but can also be typed-in manually right before loading the data.

5. reduced data: Only every nth data point of the Fabric Analyser raw
data is used for the analysis. Reducing the data will decrease the computing time significantly, but will decrease the quality of the images, too. n=2-10 is often a reasonable choice.

6. area selection: Activates rectangular data cropping. The data is cropped during the loading process. If another region is selected the data needs therefore to be loaded again.

7. x coordinate: x coordinate (in pixel) of the data cropping; origin (x=0) at the left.

8. y coordinate: y coordinate (in pixel) of the data cropping; origin (y=0) at the bottom.

9. x size: Size in x-direction of cropped region (in pixel).

10. y size: Size in y-direction of cropped region (in pixel).

Figure 5: Screenshot of the FAME main GUI with all panels visible.

11. preview: Opens preview GUI, details in section 7.2.

12. polygon selection: Activates polygonal-shaped data cropping. After starting the loading process a preview is generated and the polygonal can be drawn manually. If the polygonal closed by clicking on the first point again (a circle is shown) the actual loading process is started.

13. interior grains only: Developed to remove the troubles connected
with the irregularities in polygonal-cropped data (section 7.3). All grains are removed from the FAME grain map which centroid (equivalent to the centre of mass in geometric shapes) is outside the selected polygon.

14. polygon from file: Load the polygon coordinates from another project (mtex_import or results-file) or from a .txt file (“from .txt file” activated: [15])

15. from .txt file: Enables the import of a polygon from an external .txt file. The x-coordinates need to be in a column, separated by tab space from the y-coordinates in a second column. File is loaded using “load polygon” ([16]).

16. load polygon: Select a previously used polygon from the respective mtex_import- or results-file. If “from .txt file” ([15]) is activated the coordinates stored in a .txt file are used.

17. load: Loads the Fabric Analyser .cis file (info.txt is also necessary) and converts the data to mtex_import.n_data.txt and a mtex_import.n_data.mat (n: reduced data parameter) files. Loading is compulsory for the consecutive analysis process. It takes ≈15s (reduce data=2) for a single image of size 1000x1000 pixels. The loading of batch data is appropriately longer (e.g. ≈3 min. for 10 images).

18. no. of image(s): Displays numbers of images for 2d deformation experiments after data loading.

19. size of image(s): Displays size of image(s) after data loading. First number indicates width, second height of image; in pixel.

20. user information: Info box to inform user about ongoing processes and errors.

21. testing: Opens the testing-GUI; details in section 8.2.1.

22. gqgm filter: Geometric quality for grain map filter. Threshold for filtering out pixel with bad geometric quality (0: bad quality, 100: excellent quality) for the grain labelling. 1 is often good choice (only really bad quality is removed). For some ice experiments with unclearly defined grain boundaries switching off is a good choice. Details about the definition of the geometric quality are to be found in Peternell et al. (2009).

23. rqgm filter: Retardation quality for grain map filter. Threshold for filtering out pixel with bad retardation quality (0: bad quality, 100: excellent quality) for the grain labelling. 1 is often good choice (only really bad quality is removed). For some ice experiments with unclearly defined grain boundaries switching off is a good choice. Details about the definition of the retardation quality are to be found in Peternell et al. (2009).

24. min. radius (µm): Threshold for filtering out small grains (in µm)
from the FAME grain map during the analysis. A good choice for many applications is often 40-60.

25. **angle grain criteria**: Threshold (angle in degree) for separating individual grains during the grain labelling process. It is the most important parameter of the analysis. Details about the used grain labelling algorithm are to be found in Bachmann et al. (2001). In almost all cases between 1 and 8; often 2.5-5 is a reasonable choice.

26. **FA resolution (µm/pixel)**: Resolution of Fabric Analyser during the measurement. Especially important for the definition of the min. radius and for the statistics.

27. **angle grain criteria after deformation**: For 2d deformation experiments only. Defines the angle grain criteria after the end of deformation. Enables a better adjustment of the parameter and therefore a better grain labelling during the progress of deformation.

28. **annealing**: Activate for 2d deformation experiments with subsequent annealing for adjustment of angle grain criteria.

29. **angle grain criteria after annealing**: For 2d deformation experiments with subsequent annealing only. Defines the angle grain criteria after the end of annealing. Enables a better adjustment of the parameter and therefore a better grain labelling during the progress of deformation and annealing. “annealing” ([28]) needs to be switched on.

30. **end of deformation**: For 2d deformation experiments with subsequent annealing only. Defines the last image of deformation during deformation experiments with subsequent annealing.

31. **step growth testing**: Opens the step growth testing-GUI for finding appropriate parameters for the step growth process.

32. **grow grains**: Completely fills the empty space of the filtered small grains. In most cases a controlled growth using the step growth ([33]) is recommended.

33. **step growth**: Improved grain labelling through controlled growth of grains: Enables a pixel-wise enlargement of grains. Optional, but highly recommended to use. Details to be found in section 8.4.

34. **steps**: Number of steps the grain growth process is repeated. Use the step growth testing tool ([31]) to simplify the search for a fitting parameter.

35. **threshold**: Enables a subsequent combination of individual grains with similar orientation during the step growth process. Often useful for differentiate between subgrains.
36. **criteria**: Parameter (in degree) of the threshold for separating individual grains during the step growth process. A good choice is often 5-8.

37. **default**: Restores default parameters.

38. **analyse**: Grain labelling using the MTEX algorithm (Bachmann et al., 2011) of Fabric Analyser orientation data. Essential parameters are gqgm/rqgm filter, min. radius and angle grain criteria. If “step growth” ([32]) is activated a subsequent advanced grain labelling is performed. Final FAME grain maps are stored as .bmp files and data in a results.. .mat file with filename containing some information about the used parameters. Requires previous loading of data. Details are to be found in chapter 8.

39. **opaque grain filter**: Useful for experiments using a sopaque phase (e.g. graphite): Filters all black grains (latitude of c-axis ≥88°)

40. **show image**: Images are displayed on the screen during the analysis. Especially useful for saving the FAME grain map in a different file format.

41. **statistics**: Opens the statistics-GUI for the graphical representation of the results of the analysis.

42. **FAME2elle**: Opens the FAME2elle-GUI for generating elle (modelling software) supported .ppm files. Previous analysis required.

43. **close**: Terminates FAME and closes the main and all sub GUIs.

### 6.2 Preview-GUI

The FAME preview-GUI (Fig. 6) is displayed after pushing the “preview”-button ([11]; Fig. 5) in the main GUI.

44. **reduce data**: Only every nth data point of the raw data is used. Missing data is interpolated.

45. **gqgm filter**: Geometric quality for grain map filter. Pixel with a geometric quality filter smaller than the input threshold are coloured white in the preview image.

46. **rqgm filter**: Retardation quality for grain map filter. Like gqgm filter, but applying retardation quality filter.

47. **generate preview**: Display preview orientation image on screen with filters [44-46] applied.
48. **generate image files**: Choose type of raw data image file in the pop-up menu. Push the “generate image”-button to generate and save the appropriate image.

49. **image no.**: Select image for preview out of the batch data (batch data only).

50. **close**: Closes the preview-GUI.

Figure 7 shows a screenshot of the FAME testing-GUI. It is displayed after pushing the “testing”-button in the main GUI.
6.3 Testing-GUI

51. user information: Info box to inform user about ongoing processes and errors of the testing process.

52. gqgm range: Defines the range of the gq grain map filter. The lowest used gq filter is defined by “min”, the highest by “max”. The number is defined by “points” and values in the middle equidistantly distributed.

53. rqgm range: Like [52], but for the rqgm filter.

54. min. rad. range (µm): Like [52], but for the min. radius.

55. angle grain criteria r: Like [52], but for the angle grain criteria.

56. start testing: Starts the testing process and generates FAME grain maps with the parameter combinations defined in [52-55].

57. close: Terminates the testing-GUI.
6.4 Step growth testing-GUI

Figure 8 shows the FAME step growth testing-GUI. It appears after pushing the “step growth testing”-button in the main GUI.

Figure 8: The step growth testing-GUI.

58. user information: Info box to inform user about ongoing processes and errors of the step growth testing process.

59. total steps: The total number of growth steps applied on the current FAME grain map.

60. threshold: Enables a subsequent combination of individual grains with similar orientation.

61. criteria: Parameter (in degree) of the threshold for separating individual grains

62. number of steps: Number of growth steps going to be applied by pushing “grow”.

63. start: Loading the original FAME grain map (previous loading and analysing of data necessary!).

64. grow: Growing the existing grains. Number of steps defined by [62]. Subsequent growth steps add if grain map is not loaded anew.

65. close: Terminates the step growth testing-GUI.
6.5 Statistics-GUI

![Image of the statistics-GUI](image)

Figure 9: The statistics-GUI.

66. **user information**: Info box to inform user about ongoing processes and errors of the statistics processes.

67. **grain size statistics**: Bar diagram of equal area diameter (EAD) and grain area distribution (“2d deformation” ([3]) deactivated). In case of batch data ([3] activated) a mean EAD vs. strain rate and a combined area fraction/number of grains vs. strain rate plot is generated instead. The area fraction is defined as the area occupied by the labelled grains divided by the complete sectional area.

68. **grain shape orientation**: Rose diagram of shape preferred orientation (SPO; [3] deactivated), based on prose-plot of the open source MATLAB® toolbox PolyLX (Lexa, 2003). In case of batch data ([3] activated) a mean SPO vs. strain rate plot is generated instead.

69. **modelled grain cor.**: Grain size correction based on simple model. In the case that the grains were filtered and not regrown (“grow grains” [32] deactivated), some areas in the FAME grain map are left empty. This area is assumed to be filled with uniform distributed grains. The largest possible grains have the minimal filter radius (“min. radius”; [23]). This modelled grain distribution is used to estimate a corrected grain diameter.
70. **spherical grain cor.:** Spherical grain size correction. Corrects the (sectional) diameter to the more realistical spherical diameter, as described by Heilbronner (Heilbronner, 1992).

71. **total strain (\%)**: Indicates the final strain reached in a deformation experiment. If a subsequent annealing stage is present the annealing data is plotted on the strain-axis as well; an appropriate upscaling of the strain value is therefore necessary to ensure a correct labelling of the axis. (option only available for batch data)

72. **one grain size group**: Evaluate all grains together statistically (option only available if “step growth” is deactivated).

73. **2 grain size groups**: Dividing grains into two groups depending on grain size which are evaluated separately in the grain size and shape statistics. One group contains all grains larger than the mean equal area diameter (EAD), the other one grains with a smaller diameter. (option only available if “step growth” is deactivated)

74. **auto grain size**: Depending on a grain size criteria ([75]), FAME decides if the grains are divided into two groups or not for the statistical evaluation. (option only available if “step growth” ([32]) is deactivated)

75. **grain size criteria**: Parameter for “auto grain size”. The 2 group evaluation is favoured for a smaller value. Depends on grain area and diameter distributions. (option only available if “step growth” ([32]) is deactivated)

76. **strain axis (\%)**: Scaling of the strain-axis, independently of the highest strain reached in the experiment. Especially useful for comparing deformation experiments with different final strain on the using the same x-axis scaling. Needs to be higher than (or equal to) the “total strain”. (option only available for batch data)

77. **plot eigenvector path**: Plots the spherical projection of the orientation tensor eigenvectors. In case of single data (“2d deformation” ([3]) deactivated), the position of the eigenvector projection is indicated by a hollow circle. For deformation experiments the first position is indicated again by a hollow circle, the following points by filled circles. The colour of the circles indicates the progress of deformation: Black at the beginning, red at the end of the experiment. The appropriate eigenvector can be selected using [78].

78. **plot eigenvector no.**: Selecting the eigenvector (1, 2, 3) for the eigenvector plot ([77]). Eigenvector number 1 is the eigenvector corresponding to the largest eigenvalue, 2 for the second largest and eigenvector 3 corresponds to the smallest eigenvalue.

79. **plot ternary path**: Fabric shape represented in a ternary diagram
using eigenvalues of orientation tensor. I: Isotropy, G: Girdle, C: Cluster. See Benn (1994) for details. The start of the experiments is indicated by a circle, the beginning of the annealing by a square and the end by a triangle. The deformation path is coloured black, the path of the annealing stage red.

80. **stereographic plots:** Opens the stereographic plots-GUI (Fig. 10).

81. **kernel misorientation:** Generating a c-axis misorientation map using a 8-pixel kernel (if “kernel size 24” ([84]) is activated: 24). For details about full-crystallography misorientation maps using EBSD-data, see Wright et al. (2011). Hint: The generation of c-axis can take a while for larger data sets: A few hours are not uncommon for a e.g. 6000x3000 pixels single image!

82. **threshold:** Using only neighbouring pixels for misorientation calculation if it has a smaller c-axis misorientation relative to the central pixel than the given threshold (in degree).

83. **inside grain:** Using only neighbouring pixels for misorientation calculation if it belongs to the same labelled grain as the central pixel.

84. **kernel size 24:** Using a kernel size of 24 instead of 8, i.e. not only the 8 direct neighbours are used for calculation, but also the 16 next closest pixel.

85. **fixed:** Fixed colourscale for colouring the misorientation map. The left side of the colourbar (saved as misorientationcolourscale.bmp) corresponds to 0°, the right end to the value given.

86. **auto:** Scaling of colourbar appropriately chosen by FAME. The left side of the colourbar (saved as misorientationcolourscale.bmp) corresponds to 0°, the right end is shown in the “user information”-panel ([66]) afterwards. It is also indicated in the name of the saved misorientation image.

87. **show results:** Plots are displayed on the screen during the analysis. Especially useful for saving them in a different file format.

88. **calculate statistics:** Starting the calculation of the statistics and generating the corresponding plots. Takes in general 1-2 min. for a single data set. The c-axis misorientation is often the most time-consuming process. If stereographic plots are to be generated the corresponding GUI needs to be left open.

89. **close:** Terminates the statistics-GUI.
6.6 Stereographic plots-GUI

**Figure 10: The stereographic plots-GUI**

90. **stereographic density plot**: Generating a stereographic density plot using the orientation of the labelled grains.

91. **orientation density function**: Generating a orientation density plot using the orientation of the unlabelled pixels. The plot is based on the plotpdf function of MTEX (Bachmann et al. 2011).

92. **Schmidt diagram**: Plotting the orientation of each labelled grain using the stereographic Schmidt projection (Schmidt, 1925).

93. **small circle count**: Interpolating the data for the stereographic density plot using the small circle count method (Mellis, 1941).

94. **small circle area (%)**: Area of the circles used in the small circle count method; in percent of the whole area.

95. **grid size (50-1000)**: Size of the grid parameter for the small circle count method. Should be between 50 and 1000.

96. **fisher distribution**: Interpolating the data for the stereographic density plot using the Fisher distribution (Fisher et al. (1993), p. 86-88).

97. **kappa (50-1000)**: Shape parameter $\kappa$ used for the fisher distribu-
tion, see Fisher et al. (1993) (p. 86) for details. Should be between 0 and 100.

98. **gq filter**: Geometric quality filter. Threshold for filtering out pixels with bad geometric quality (0: bad quality, 100: excellent quality) for the orientation density function. See Peternell et al. (2009) for details.

99. **rq filter**: Retardation quality filter. Threshold for filtering out pixels with bad retardation quality (0: bad quality, 100: excellent quality) for the orientation density function. See Peternell et al. (2009) for details.

100. **colorbar const.**: Fixed colourbar scaling for the stereographic density plots. Values indicating (dimensionless) orientation density. If switched off, colourbar is appropriately scaled automatically.

101. **contour lines**: Plotting stereographic density plot with black contour lines.

102. **show colourbar**: Colourbar is plotted next to the stereographic density plot. If switched off, it is saved in separate image file.

103. **colorbar 2**: A different colourbar is used to visualise the orientation density in the stereographic density plot.

104. **plot eigenvectors**: Plotting the position eigenvectors in the stereographic density plot and the orientation density function.

105. **plot mean**: Plotting the position of the mean density in the stereographic density plot and the orientation density function.

106. **close**: Terminates the stereographic plots-GUI-GUI.
6.7 FAME2elle-GUI

Figure 11: The FAME2elle-GUI.

107. user information: Info box to inform user about ongoing processes and errors of the FAME2elle process.

108. large grain seeding: Fill non-labelled regions with newly seeded grains. Grain size of the seeded grains is normally distributed with mean and standard deviation from the FAME microstructure (Hammes and Peternell, in press).

109. wrapping boundaries: Enforce wrapping boundary conditions: Grains at the top and left edge are mirrored to the bottom and right, and the corresponding grains are replaced (Hammes and Peternell, in press).

110. small grains filter: Filtering out all grains smaller than the value given by [111].

111. small grains filter: Filter threshold for [110].
112. **final image size:** Pixel size of converted grain map image. Hint: A 1024x1024 has 64 times the size of a 128x128 image and is therefore expected to take roughly 64x the time to generate!

113. **use external orientation data:** Getting orientations for the newly seeded grains from an external file. See chapter 10 for details about the required structure. If switched off, orientation is random.

114. **convert:** Generate the ppm-files for the elle-modelling software. A ppm2.txt-file containing the coordinates and orientation of each pixel and a ppmfileheader.txt containing the orientation of each grain are produced. In addition, an orientation map (ppmrgb.bmp) is saved. About the required time of the conversion process see chapter 10 and the comment to [112]. Remember: The conversion is NOT deterministic, due to the random locations and random orientations of the newly seeded grains. Therefore, the ppmrgb.bmp images produced are expected to be different each time they are generated!

115. **close:** Terminates the FAME2elle-GUI.
Chapter 7

Loading data

The microstructure data recorded by the Fabric Analyser is stored in a binary file without a header (data.cis).

Figure 12: a) Example of a folder containing a batch experiment. b) Folder containing Fabric Analyser data after loading. The log-folder contains the log.txt file where e.g. finished processes are listed. The data.cis and info.txt are the Fabric Analyser raw data files. c) Content of the results-folder. All further files generated by the analysis, statistics or FAME2ELLE processes will be stored there. In case of single data the folder structure shown in (a) is not necessary.
To get information about the size of the image FAME also needs a info.txt file.

If batch data (2d deformation experiment) is used the two files have to be in a separate numbered folder for every slide (Fig. 12a). If a lower number (e.g. “1”) has less digits than another (e.g. “100”), insert zeroes to achieve a equal length of all numbers (e.g. “001”). Otherwise deformation data sets won’t be ordered, which will result in faulty statistical analysis.

The loaded data can be generally reduced (“reduce data”) by using only every nth. pixel (missing data is interpolated) or cropped by a rectangular or polygonal shape (section 7.3).

The loading process reads the Fabric Analyser data.cis binary file (Fig. 12b) and converts it into FAME-readable data structure. A mtex_import_n_data.txt and a mtex_import_n_data.mat files are generated (Fig. 12c); n is the grade of data reducing. The data structure is identical to the files in the original FAME scripts, details are are to be found in Peternell et al. (2014). The generated files are used for the grain labelling during the analysis (chapter 8).

The loading process takes ≈15s (reduce data=2) for a single 1000x1000 image and appropriately longer in the case of batch data (e.g. ≈3 min. for 10 images).

If a new project is started using data which were already loaded (or analysed) before, the files in the results-folder are in general being replaced. Saving your results by copying the data is therefore recommended!

7.1 How to load data?

Here the FAME data loading using is explained step-by-step. Numbers in brackets [] refer to the respective positions of the panels/buttons in figure 5. Compulsory steps (1, 2, 5) are underlined and optional ones can be skipped (3, 4). The preview-tool and the data cropping tools are discussed in detail in figures 10 and 12, respectively.

**Step 1: Select data type.** Activate “2d deformation experiment” ([3]) in the case of batch data. Switch off if only single data is used.

**Step 2: Select data.** Pushing the “new project”-button ([1]) opens a file browser. Select the data.cis-file of the experiment to be analysed. In the case of a deformation experiment data it is irrelevant which of the .cis-files is selected. A new project can be opened at any time in FAME, unless a process is running. After a data set was chosen successfully the preview-tool can be used (section 7.2).
Figure 13: Workflow of the FAME data loading. Numbers in brackets [] refer to the respective positions in the main GUI (Fig. 5)
Step 3: Reduce data. Type in an integer n into “reduce data” ([5]) to decide if only every nth data pixel is to be used. n=2 is in many cases a reasonable choice.

Step 4: Data cropping. Select a rectangular or/and polygonal shaped image region by using [6-10] or/and [12-16], respectively. For details refer to figure 17.

Step 5: Start loading. Simply push the “load”-button. If “polygon selection” ([12]) was activated, the polygon needs to be drawn first (section 7.3). The loading process should take ≈15s (reduce data=2) for a single 1000x1000 image and appropriately longer in the case of batch data (e.g. ≈3 min. for 10 images). The generated files are stored in the results-folder (Fig. 12a).

Now the Fabric Analyser data should be successfully loaded into FAME and ready to be analysed (chapter 8).

7.2 Preview

The preview tool is used to visualise Fabric Analyser raw data orientation images with rqgm/gqgm filter (geometric/retardation quality grain map filter) and reduced data applied for choosing the rqgm/gqgm filter and reduce data parameters (“generating preview”; example: Fig. 14a). The preview image is directly displayed on screen and no file is saved.

In addition, orientation, gq/rq and retardation (example: Fig. 14b) images can be generated from the Fabric Analyser .cis file (“generating image files”), if not already existing.
7.2.1 How to use the preview tool?

In figure 15 the workflow for preview-tool is shown. Numbers in brackets \([\text{11}]\) refer to the respective positions in the preview-GUI (Fig. 6).

**Step 1: New project.** Opening a new project (Fig. 13: Step 1 and 2) is necessary to use the preview tool.

**Step 2: Open preview-GUI** Push “preview” ([11]) in the main GUI.

**Step 3: Generate preview** Select parameters [44-46] and push [47]. A preview with the applied filter options will be generated and displayed on the screen.

**Step 4: Generate image files** Select an image type in the drop down menu and generate the appropriate file by pushing “generate image” ([48]). It will be saved next to the corresponding .cis-file.
7.3 Data cropping

The FAME data cropping enables the selection of a user-defined region of the Fabric Analyser data.

A rectangular data selection is possible using the “area selection” ([6-10] in fig. 5). Origin of the coordinate system (x=0, y=0) is at the lower left corner. Using the preview-tool (section 7.2; Fig. 15) is often quite useful to define the proper coordinates. Figure 16c shows a FAME grain map generated from a rectangular region selected from the original data (Fig. 16a).

In addition to the rectangular crop, a polygonal-shaped crop (“polygon selection”) is possible. After starting the loading process a preview is generated and the polygonal can be drawn manually. If the polygonal is closed by clicking on the first point again the actual loading process is started. The polygon can also be acquired from a different FAME project using “polygon from file”. In addition, the coordinates of a polygon can also be loaded from an external .txt-file (“from .txt file”). In the file x-coordinates needs to be in a column, separated by tab space from the y-coordinates in a second column. Figure 16f) shows an simple example how the .txt-file should look like.

Keep in mind that polygonal-cropped data sometimes lead to irregularities at the outer boundaries, due to partly cut-off grains (Fig. 16d). To fix this problem, the “interior grains only”-option was developed. Unlike the simple polygonal selection the raw data is not cropped, but grain labelled first. Then all grains are removed from the FAME grain map which centroid (equivalent to the centre of mass in geometric shapes) is outside the selected polygon. Therefore, no cut-off grains occur. Figure 16d)/e) show a
region selected using the “interior grains only” (e), in contrast to the simple polygonal selection (d).

Figure 16: a) Fabric Analyser Orientation image of part of a quartzite section. The polygonal shape is used for data cropping. b) FAME grain map of (a). c) FAME grain map of rectangular region cut from (a). d) Polygonal region cut from (a) and grain labelled. e) Like (d), but “interior grains only” activated. Parameters used for b)-e): gqgm/rqgm=1, min. radius=56.67, angle grain criteria=4.11; step growth activated (5 steps, criteria=5). f) Example how a .txt-file with coordinates of a polygon should look like.

7.3.1 How to crop data?

Here the data cropping using FAME is explained step-by-step. The crop tools are part of the data loading, for details refer to fig. 17. Numbers in brackets [] refer to the respective positions of the panels/buttons in the main GUI (Fig. 5).
Figure 17: Workflow of the FAME data cropping. Numbers in brackets [] refer to the respective positions in the main GUI (Fig. 5)

**Step I: New project.** Opening of a new project is required to be done prior to the data cropping. See figure 13 for details.

**Step: II: Area selection.** Switch on [6] if a rectangular region crop is desired. Input coordinates (origin at lower left) in [7-10].

**Step: III: Polygonal crop.** Activate [12] for a polygonal shaped crop. If only complete grains are to be selected, switch on [13]. A combination of polygonal selection with the rectangular area selection is also possible.
Step: IV: Polygonal from file. By switching on [14] the polygon of another project can be loaded from the corresponding .mat-file or the coordinates from a .txt-file (Steps Va and VIa). If a manual selection of a polygon is desired, switch off [14] and go to step Vb.


Step: Vb: Load data. If the polygon is manually selected, the data loading process ([17]) needs to be started first. See figure 13 for details.

Step: Vb: Draw polygon. After [17] is pushed (and [14] deactivated) a preview image is displayed on screen. The generation of the image can take a few seconds, therefore, please be patient! The polygon can now be manually drawn by clicking on the displayed image (Fig. 18a). If the polygonal is closed (a circle is displayed: Fig. 18b) by clicking on the first point again the actual loading process is started.

Figure 18: Manually draw a polygonal shape (a) for selecting a region for cropping. The process if completed by clicking on the first point again; a circle symbol appears by hovering over the right spot.
Chapter 8

Analysing data

The data analysis represents the heart of FAME: The initial pixel data recorded by the Fabric Analyser is grain labelled to enable a statistical evaluation of the fabric structure. The grain labelling operation uses the Voronoi decomposition based MTEX algorithm (Bachmann et al., 2011).

The analysis depends crucially on a set of parameters which significantly influence the grain labelling (see following sections). A carefully considered choice is therefore of outstanding importance for a successful fabric evaluation.

A previous loading of the data is required to execute the analysis (chapter 7). The actual analysis operation, started by pushing “analyse” in the main GUI ([38]; Fig. 5), produces two files: A results.mat- and grainmap.bmp-file. In both cases the actual filename contains information about the most important of the used parameters. They will be stored in a results-folder next to the Fabric Analyser .cis-file. The .mat-file can only be opened by using the MATLAB® environment and contains information all necessary information for plotting the statistics (chapter 9). Furthermore, it is the basis for generating the files for the ELLE-modelling software (chapter 10).

The processing time the analysis is difficult to evaluate and depends on many factors. However, most influential are the image size (in pixel) and the “reduce data” (chapter 7). The analysis of a single image of 1000x1000 pixels with reduce data=2 applied should takes \( \approx 3-7 \) minutes. In some exceptional cases, the process can be more time consuming. In general, an increased “reduce data” value or the selection of a smaller area (crop data: section 7.3) leads to a considerable reduction of the processing time.

The progress of the analysis is shown in a specific “progress”-window, which is displayed in the upper left corner of the screen (Fig. 19). Process 1 corresponds to the MTEX grain segmentation, 2 to the conversion of the
MTEX grains to the FAME grain map and process 3 is the (optional) step growth.

Figure 19: Window for tracking progress of analysis process.

By activating “show grain map” the generated FAME grain map is directly displayed on the screen (Fig. 20). This is in particular useful for saving the grain map in a different file format. Simply go to the “floppy disk”-symbol (arrow in fig. 20), select a proper file format and save it in the desired folder.

Figure 20: FAME grain map displayed on screen. Arrow indicates position to save grain map in different file formats.

8.1 How to analyse data?

In this section the user is introduced into the FAME data analysis step-by-step. Numbers in brackets [] refer to the respective positions of the panels/buttons in figure 5. Compulsory steps (1, 4, 5) are underlined and
optional ones can be skipped (2, 3). The testing and the step growth testing-tools are discussed in detail in figures 22 and 26, respectively.

**Step 1A: Load data.** Previous data loading is required. See figure 13 for details.

**Step 1B: Open Project.** In addition to loading the data of a new project, an already existing project can be opened. Simply push “open project” ([2]) and select a mtex_import_n_data.mat- (loaded, not analysed) or results.mat- (already analysed) file. If a change in the “reduce data”-parameter or another region of interest (area selection or polygon selection) is wanted, a new project needs to be opened and the data loaded anew.

**Step 2: Testing.** For most cases a determination of the basic input parameters is necessary. Usage of the testing-tool is recommended (section 8.2.1).
Figure 21: Workflow of the FAME analysis. Numbers in brackets [] refer to the respective positions in the main GUI (Fig. 5).

**Step 3: Input parameters.** Please input the basic input and 2d parameters into panels [22-26] and [27-30]. Further details about the “basic input parameters”, “2d deformation” see sections 8.2 and 8.3, respectively. All parameters can be set back to default, using button [37].
Step 4: Step growth testing. The step growth parameters can be easily provided using the step growth testing-tool (section 8.4).

Step 5: Input step growth parameters. Please input the step growth parameters into panels [32-36]. Further details about the step growth are found in the respective section below (8.4). All parameters can be set back to default using button [37].

Step 5: Analysis. Start the analysis by pushing [38]. A .mat- and a grainmap.bmp-file will be generated in the results-folder. This will take a few minutes for a single image of size 1000x1000 pixels.

8.2 Basic input parameters

The gqgm/rqgm, min. radius and the angle grain criteria are most important for the FAME analysis. The FA resolution has no influence on the actual grain labelling but is necessary for statistical evaluation, especially for the mean grain size (chapter 9).

The gqgm (geometric quality for grain map) filter sets a threshold for filtering out pixel with bad retardation quality (0: bad quality, 100: excellent quality) for the grain labelling. The rqgm (retardation quality for grain map) filter is equivalent to the gqgm filter, but based on the retardation quality. Details about the definition of the retardation and geometric quality are described by Peternell et al. (2009). The influence of the gqgm/rqgm filter on a data set can be visualised using the preview-tool (section 7.2). In many cases setting gqgm/rqgm filter to 1 (only really bad quality is removed). For some ice experiments with unclearly defined grain boundaries switching off both filter is a good choice.

The min. radius filter sets a threshold for filtering out small grains (in µm) from the FAME grain map. A good choice for many applications is 40-60, but the actual value depends on the fabric of the sample.

The angle grain criteria is clearly the most important of the input parameters. It sets the threshold (angle in degree) for separating individual grains during the grain labelling process. In most cases the angle grain criteria has a value between 1 and 8. Often 2.5-5 is a good choice. The processing time of the analysis often increases for an angle grain criteria ≤1.5.

8.2.1 Testing

As discussed in the last section, the gqgm/rqgm filter, min. radius and the angle grain criteria influence the grain labelling of the analysis significantly. It is a time consuming work to find appropriate parameters to get
a FAME grain map which describes the crystallographic state properly. To ease this task the testing-tool was developed.

The testing-tool generates FAME grain maps with different combinations of the 4 parameters crucial for analysis (gqgm, rqgm, min. radius and angle grain criteria). The images are saved in the testing-folder next to the corresponding .cis-file. The generation of a single “test”-grain map takes in general less time than a full-sized analysis, but usually not only one image is produced! A rough approximation of the required time is shown in the “user information”-box in the testing-GUI ([51]; Fig. 7), after the parameters are entered. In some cases errors occur during the grain labelling. If this happens the corresponding FAME grain map is not saved in file and the “user information”-box in the testing-GUI ([51]; Fig 7) notifies about the event (e.g. “1 error(s)”). In almost all cases this is based on the fact that the used parameters results in a grain map where all grains are filtered out! This mostly happens with a rather small angle grain criteria ($\leq 1.3$) in combination with a larger min. radius (e.g. $\geq 50$).

After the “testing”-grain maps were generated, the know-how and experience of the user is required to compare the resulting FAME grain map with the orientation image. In this way a proper set of parameters is obtained.

It is recommended to run the testing-process overnight. The generation of 100 grain maps (size: 1000x1000 pixels, reduce data=2), takes $\approx 10$h. In many cases the gqgm and rqgm filter values are of lesser importance than the other parameters. They are often set both to 1 (in exceptional cases set to 0). A reasonable approach is to select a wider range of min. radius (e.g. 10-150, 10x) and angle grain criteria (e.g. 2-8, 10x). A second testing-round with narrower parameter ranges can be quite useful for a more refined determination of the parameters.

### 8.2.1.1 How to use the testing-tool?

In this section the user is introduced into finding fitting parameters for the subsequent analysis using the testing-GUI. Numbers in brackets [ ] refer to the respective position of the panels/buttons in figure 7).

**Step 1A: Load data.** Previous data loading is required. See figure 13 for details.

**Step 1B: Open Project.** In addition to analysing the data directly, an already existing project can be opened. Simply push “open project” ([2]) and select a mtex_import- or results.mat file.
Step 2: Open testing-GUI. Push “testing” ([21]) in the main GUI.

Step 3: Select parameter range. Select the range of parameter in [52-55]. The lowest value defined by “min”, the highest by “max”. The number of points is defined by “number”, and values in the middle are equidistantly distributed. If a parameter is wished to be constant, please type in “1” in “points”. Testing a wide range of parameters is time consuming, generating ≈ 100 FAME grain maps (size: 1000x1000 pixels) will usually take overnight. Remember that the angle grain criteria is the most
crucial parameter and therefore needs to be varied extensively! \( gq/rq \) are in most cases set to 1.

**Step 4: Start testing.** Please, push the “start testing”-button ([56]). FAME grain maps with the parameter combinations defined in [52-55] are generated. Depending on the number of chosen parameter combinations (and the image size) this can take a few minutes, hours or VERY long!

**Step 5: Evaluate test images.** Compare the generated FAME grain maps with the non-labelled orientation map and decide which fits best (example: Fig. 23).

**Step 6: Adjust parameter ranges.** If an appropriate FAME grain map was found in step 5, it is often recommended to go back to step 4 and narrow the parameter ranges to find an even better one!

### 8.2.1.2 Example

Figure 22b shows the 9 test images generated during the testing-tutorial. The \( gg\) and \( rq\) filter were both hold constant at 1. The minimal was radius varied from 10 to 150 and the angle grain criteria from 2 to 8; for both parameters 3 points each. For finding proper parameters the test images needs to be compared with the orientation image (Fig. 23a)

A min. radius of 150 filters out some small, but still realistic grains. On the other hand, a min. radius of 10 is possibly too small, considering the many small grain fragments between the larger grains (circles in middle left image). These small fragments will influence the grain size statistics significantly and in most cases doesn’t represent real grains. A reasonable min. radius filter will therefore be somewhere between 10 and 80. For the angle grain criteria a value of 8 seems to be too large, because a couple of obviously different grains were labelled as part of larger grains (“x” in lower left image). Here a value between 2 and 5 seems to be a better choice. The next step would be testing with narrower parameter ranges, for example 25-65 for the min. radius and 2.5-4.5 for the angle grain criteria.

A more elaborate testing would show that a min. radius of 56.67 and an angle grain criteria of 4.11 lead to good results.
Figure 23: a) Fabric Analyser orientation image of the tutorial example. b) Testing tool applied on the image shown in (b). \( gq=1, \) \( rq=1, \) min. rad. = 10-150 (3x), angle grain criteria=2-8 (3x). Circles and “x”: see text.
8.3 2d deformation (batch data)

FAME also enables the processing of 2d deformation experiments with multiple (batch) data sets. Examples of this analysis can be found in Wilson et al. (2014) and Peternell et al. (2014, in press) In this case, further user input (“2d deformation”: [27-30]; Fig. 5) is required. To facilitate a proper grain labelling during the progress of deformation, the applied angle grain criteria is adjusted. The data in the first folder (data structure of 2d
deformation experiments: chapter 7) is analysed using “angle grain criteria” ([24]) and the last folder uses the value given by “angle grain criteria after deformation” ([27]). In between, the applied angle grain criteria is linearly interpolated. In the case of deformation experiments with a subsequent annealing, the applied angle grain criteria is likewise adjusted, starting with “angle grain criteria after deformation” and ending with “angle grain criteria after annealing”. The number of the last folder of the deformation is given by “end of deformation”. This number is obtained by counting the folders belonging to the deformation stage, independent of the name of the folder itself.

8.3.1 How to analyse batch data?

Here the user is explicitly introduced into the analysis of 2d deformation experiments (batch data). Differences to the analysis of single data are emphasised. Numbers in brackets [] refer to the respective position of the panels/buttons in figure 5. Compulsory steps are underlined.

Step 1A: Load data. Previous data loading is required. In contrast to single data “2d deformation” ([3]) needs to be activated before opening a new project. It is of no importance which of the .cis-files is selected. See figure 13 for further details.

Step 1B: Open Project. In addition to analysing the data directly, an already existing project can be opened. Simply push “open project” ([2]) and select a mtex_.import- or results.mat file.

Step 2: Testing. The basic parameters for the first and the last image of a deformation experiment are needed. Simply apply the testing-tool on these two data sets, like for single data. In case of a subsequent annealing, the parameters after the end of the actual deformation are also necessary. Except the angle grain criteria, all parameters are constant for all parts of the experiment. See section 8.2.1 for further details about the testing-process.

Step 3: Step growth testing. Similar to the testing-process, the step growth parameters (steps, criteria) are constant and therefore needed to be selected wisely. See section 8.4 for further details about the step growth testing.

Step 4: Input. Input the basic, 2d deformation and step growth parameters into the main GUI. For details about the “end of deformation” parameter, see main text to this section (above).

Step 5: Analysis. Start the analysis by pushing [38].
8.4 Step growth

Small grains below the grain size threshold ("min. radius") lead to non-labelled (white area in fig. 25a) areas in the FAME grain maps. In many cases the size of the grains are underrepresented, and a process to increase the grain size, in addition to filling holes, is desirable. The simplest approach is to grow the grains until they completely fill all remaining areas ("grow grains"; [32] in fig. 5; example: 25b). This often leads to the other extreme, an overestimation of the grain size. A more selective process would be a step-wise growing of the labelled grains (Fig. 25c). For this reason the step growth-tool was developed. In one growth-step the grains grow on pixel into the neighbouring empty space. This process can be repeated multiple times ("steps"; [34]; Fig. 5). In addition to a step-wise growing, a subsequent merging of individual grains with similar orientation ("threshold"; [35]) into a new single grain is possible: Neighbouring grains with an orientation difference (in degree) below a given "criteria" ([36]) are combined. The step growth provides therefore an improved user-controlled grain segmentation.

Figure 25: a) FAME grain map of 1a. b) like (a), but with "grow grains" activated. c) Like a), but using step growth (5 steps, criteria=5); Applied parameters in a)-c): ggpm/rrgm=1, min. radius=56.67, angle grain criteria=4.11. The one pixel wide, white grain boundaries in b) and c) are generated after growth to enhance the contrast in the grain map. They are not considered in the statistical evaluation.

8.4.1 Step growth testing

To determine the necessary parameters (number of steps, threshold criteria) for the step growth-process the step growth testing-GUI (Fig. 8) is used. Further details are to be found in the following section and the accompanying figure 25.
8.4.1.1 How to use the step growth testing-tool?

Figure 26: Workflow of the FAME step growth testing. Numbers in brackets [] refer to the respective positions in the main- (Fig. 5) or step growth testing-GUI (Fig. 8)
Here the user is introduced into finding the step growth parameters (steps, threshold criteria) using the step growth testing-GUI (Fig. 8). Numbers in brackets [] refer to the respective position of the panels/buttons in figure 5 or figure 8, respectively.

**Step 1A: Load data.** Previous data loading is required. See figure 13 for details.

**Step 1B: Open Project.** In addition to analysing the data directly, an already existing project can be opened. Simply push “open project” ([2]) and select a mtex_import- or results.mat file.

**Step 2: Input parameters.** If not already done, please input basic input parameters into panels [22-26] of the main GUI.

**Step 3: Open step growth testing-GUI.** Push “step growth testing” ([31]) in the main GUI.

**Step 4: Input threshold.** Input threshold criteria in [61], if preferable.

**Step 5: Start step growth testing.** Push [63] to generate and display the FAME grain map image without applied step growth. Note: Depending on image size, the generation of the image normally can take a few minutes.

**Step 6: Grow labelled grains.** Adjust number of applied step growth steps in [62] and push [64] to start growing. The growth-process in general takes less than a minute.

**Step 7: Repeat growing.** Compare grown FAME grain map with orientation image and repeat step 6, if another growth-step is desired.

**Step 8: Adjust criteria.** If the grain labelling is not satisfactory to the user (e.g. subgrains are labelled as independent grains etc.), the threshold criteria should be adjusted and the step growth reseted by pushing “start” again. Note: Separately labelled grains are divided by a white line.
Chapter 9

Statistics

FAME offers a multitude of different diagrams to visualise the analysed data.

The plots and associated options are discussed together with the statistics- and stereographic plots-GUI (sections 6.5 and 6.6). Therefore, only examples are shown here (Fig. 27, 28). Two of the plots are only available for single data (grain size bar and SPO rose diagram; Fig. 27a/b), a couple of others only for 2d deformation batch data (variable vs. strain; Fig. 27c-e). Nevertheless, the bulk of tool can be applied on both types of data (Fig. 27). For the eigenvector and ternary path diagrams (Fig. 28e,f) only one data point will be plotted in case of single data.

If a plot is wished to be saved in a different file format, activate the “show results” button ([87]; Fig. 9) to display all generated figures on screen and save the required one manually. The procedure is identical to saving the FAME grain map in a different format (Fig. 20).
Figure 27: Grain geometry diagrams generated by the FAME statistics tool. Bar diagram of equal area diameter (EAD) and grain area distribution (a) and Rose diagram of shape preferred orientation (b) from the tutorial example (“TutEx”; FAME grain map: Fig. 1b). Mean grain size (c; EAD: equal area diameter), combined area fraction/number of grains vs. strain rate plot (d) and mean SPO vs. strain rate plot from the deformation example (“DefEx”; FAME grain maps: Fig. 2c,d). The dotted lines in c) and e) indicate the accuracies of the corresponding variables.
Figure 28: $c$-axis-plots of the FAME statistics tool. Stereographic density plot (a; Fisher distribution, $\kappa=10$), orientation density function (b), Schmidt diagram (c) and $c$-axis misorientation map (d; threshold=10, kernel size 24, colouring scale=10) from the tutorial example (“TutEx”; FAME grain map: Fig. 1b). Eigenvector path (e; eigenvector 1) and ternary path (f) from the deformation example (“DefEx”; FAME grain maps: Fig. 2c,d). Colour in (e) indicate progress of deformation (black to red). The start is indicated by a hollow circle. The start of the experiment is indicated in b) by a circle and the end by a triangle. I: Isotropy, G: Girdle, C: Cluster fabric.
9.1 How to use the statistics-tools?

Here the user learns to generate plots from the analysed data. Numbers in brackets [ ] refer to the respective positions of the panels/buttons (chapter 6).

Figure 29: Workflow of the FAME statistics-tool. Numbers in brackets [ ] refer to the respective positions in the FAME GUI’s (chapter 6).

**Step 1A: Analysing data.** Previous data analysing is required. See figure 21 for details.

**Step 1B: Open Project.** In addition to analysing the data directly, an already existing project can be opened. Simply push “open project” ([2]) and select a results.mat file.

**Step 2: Open statistics-GUI.** Push “statistics” ([41]) in the main GUI.

**Step 3: Grain geometry options.** Select the favoured options in the
statistics-GUI, regarding the gran geometry plots: [67-76].

**Step 4:** *c-axis orientation options.* Switch on [77] and [79] for the c-axis path plots. [78] selects the eigenvector.

**Step 5:** Open stereographic plots-GUI. If any stereographic plots are wanted, please push [80] in the statistics-GUI.

**Step 6:** Stereographic options. Input options in the stereographic plots-GUI. Hint: Don’t close the GUI, otherwise no stereographic plots will be generated!

**Step 7:** *c-axis misorientation options.* Input options for the generation of misorientation maps in the statistics-GUI: [81-86].

**Step 8:** Statistics. Start generating the statistic plots by pushing [88]. The selected diagrams will be saved in the results-folder as .jpg-files. The process takes in general 1-2 min. for a single data set. The c-axis misorientation is often the most time-consuming process!
Chapter 10

FAME2elle

elle (Bons et al., 2008) is a useful software for the modelling of micro-
dynamical simulations. The FAME2elle tool enables the export of FAME
data to the elle-supported ppm format. A conversion of the microstructure
is necessary to meet the elle requirements. For example elle doesn’t sup-
port non-defined regions. The non-labelled regions in the FAME grain map
(white areas in fig. 1b therefore need to be filled by grains. The FAME2elle
conversion tool fulfils this requirement by seeding new grains and fills the
remaining space by a growth process. In addition, grains smaller than a
specific value needs to be merged with a neighbouring grain. Furthermore,
no quadruple junctions (single points where four neighbouring grains met)
and “island grains” (grains completely surrounded by another grain) needs
to be removed. If wished for by the user, wrapped boundary conditions can
be imposed as well. FAME2elle tries to fulfill the set requirements with as
least change as possible in the microstructure. See section 6.7 for a descrip-
tion of the possible options of the FAME2elle-GUI. Further details about
FAME2elle are to be found in Hammes and Peternell (in press).

In addition to assuming a random or predefined (e.g. from EBSD) ori-
entation of the newly seeded grains, the orientations also can be obtained
from an external .txt-file (eulerdata.txt). It needs to be located next to the
.cis-file and contains the 3 euler angles in columns, separated by a single tab
(similar to the polygon coordinates: Fig. 16f).

By pushing “convert” ([114]; Fig. 11) FAME2elle generates the necessary
ppm-files. A ppm2.txt-file containing the coordinates and orientation of each
pixel and a ppmfileheader.txt containing the orientation of each grain are
produced. In addition, a orientation map (ppmrgb.bmp) is saved. Fig. 30
shows an example of a ppmrgb.bmp-file produced from the tutorial example
data.
The time necessary to convert the FAME grain map to the ppm format is approximately proportional to the size of the grain map image ([113]; Fig. 11). A 128x128 image should take less than 2 minutes to be produced. Therefore, a 1024x1024 (64 times the size!) image will therefore take more than 2 hours! Furthermore, a FAME grain map with a larger number of grains will also take more time to convert than a grain map with fewer grains.

Due to the random locations and random orientations of the newly seeded grains, the conversion process is NOT deterministic. Therefore, the ppmrgb.bmp images produced are expected to be different each time they are generated!

In some rare cases not all set requirements on the converted microstructure could be fulfilled by FAME2elle. If this happened the message “error occurred” is shown in the FAME2elle info-box ([107]; Fig. 11) and a special ELLElog.txt-file is saved next to the usual famelog.txt-file. In the ELLElog.txt-file all requirements are listed to notify which of those couldn’t be fulfilled successfully. Repeating the conversion (remember: partly random controlled process!) usually will produce a valid converted grain map.

10.1 How to convert data?

Here the user is introduced how to convert FAME data to elle-supported ppm files. Numbers in brackets [ ] refer to the respective positions of the panels/buttons in figures 5 and 11.
Figure 31: Workflow of the FAME2elle tool. Numbers in brackets [ ] refer to the respective positions in the main- or FAME2elle-GUI (Fig. 5, 11).

**Step 1A: Analysing data.** Previous data analysing is required. See figure 21 for details.

**Step 1B: Open Project.** In addition to analysing the data directly, an already existing project can be opened. Simply push “open project” ([2]) and select a results.mat file.

**Step 2: Open FAME2elle-GUI.** Push “FAME2elle” ([42]) in the main GUI.

**Step 3: Input options.** Input the favoured options in the FAME2elle-GUI.

**Step 4: Convert to elle.** Start the data conversion by pushing [114]. Two .txt-files (ppm2.txt, ppmfileheader.txt) and an image file (ppmrgb.bmp) are produced. See text above for details about the required processing time.


